



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Miller, Samuel I.
- (ii) TITLE OF THE INVENTION: SALMONELLA SECRETED PROTEINS
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 47
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson, P.C.
(B) STREET: 225 Franklin Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: US
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows95
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/068,804
(B) FILING DATE: 14-MAY-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US96/18504
(B) FILING DATE: 14-NOV-1996

(A) APPLICATION NUMBER: 60/006,733
(B) FILING DATE: 14-NOV-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Fraser, Janis K.
(B) REGISTRATION NUMBER: 34,819
(C) REFERENCE/DOCKET NUMBER: 00786/292002
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-542-5070
(B) TELEFAX: 617-542-8906

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCAAAGCCG	AGGAAACGAA	CCGCATTATG	GGATGTATCG	GGAAAGTCCT	CGGCGCGCTG	60
CTAACCATTG	TCAGCGTTGT	GGCCGCTGTT	TTTACCGGTG	GGGCGAGTCT	GGCGCTGGCT	120
GCGGTGGGAC	TTGCGGTAAT	GGTGGCCGAT	GAAATTGTGA	AGGCGGCGAC	GGGAGTGTCG	180

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TTTATTTCAGC	AGGCGCTAAA	CCCATTATG	GAGCATGTGC	TGAAGCCGTT	AATGGAGCTG	240
ATTGGCAAGG	CGATTACCAA	AGCGCTGGAA	GGATTAGCG	TCGATAAGAA	AACGGCAGAG	300
ATGGCCGGCA	GCATTGTTGG	TGCGATTGTC	GCCGCTATTG	CCATGGTGGC	GGTCATTGTG	360
GTGGTTCGAG	TTGTCGGGAA	AGGCGCGGCG	GCGAACTGG	GTAACGCGCT	GAGCAAAATG	420
ATGGGCGAAA	CGATTAAAGAA	GTTGGTGCCT	AACGTGCTGA	AACAGTTGGC	GCAAAACGGC	480
AGCAAACCTCT	TTACCCAGGG	GATGCAACGT	ATTACTAGCG	GTCTGGGTAA	TGTGGGTAGC	540
AAGATGGGCC	TGCAAACGAA	TGCCTTAAGT	AAAGAGCTGG	TAGGTAATAC	CCTAAATAAA	600
GTGGCGTTGG	GCATGGAAGT	CACGAATACC	GCAGCCCAGT	CAGCCGGTGG	TGTTGCCGAG	660
GGCGTATTTA	TTAAAAATGC	CAGCGAGGCG	CTTGCTGATT	TTATGCTCGC	CCGTTTGGC	720
ATGGATCAGA	TTCAGCAGTG	GCTTAAACAA	TCCGTAGAAA	TATTTGGTGA	AAACCAGAAG	780
GTAACGGCGG	AACTGCAAAA	AGCCATGTCT	TCTGCGGTAC	AGCAAAATGC	GGATGCTTCG	840
CGTTTTATTTC	TGCGCCAGAG	TCGCGCATAA				870

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTAATTA	GTAATGTGGG	AATAAATCCC	GCCGCTTATT	TAAATAATCA	TTCTGTTGAG	60
AATAGTTCAC	AGACAGCTTC	GCAATCCGTT	AGCGCTAAAG	ATATTCTGAA	TAGTATTGGT	120
ATTAGCAGCA	GTAAAGTCAG	TGACCTGGGG	TTGAGTCCTA	CACTGAGCGC	GCCTGCGCCA	180
GGGGTATTAA	CGCAAACCCC	CGGAACGATC	ACGTCCTTTT	TAAAAGCCAG	TATTCAAAAT	240
ACCGACATGA	ATCAGGATTT	GAATGCTCTG	GCAAATAATG	TCACGACTAA	AGCGAATGAG	300
GTTGTGCAAA	CCCAGTTACG	CGAGCAGCAG	GCAGAAGTCG	GAAAGTTTTT	TGATATTAGC	360
GGAATGTCTT	CCAGTGCCGT	TGCGCTGTTG	GCTGCCGCGA	ATACGTTAAT	GCTGACGTTG	420
AACCAGGCTG	ATAGCAAAC	GTCTGGTAAG	TTGTCTATTG	TCAGTTTTGA	TGCAGCTAAA	480
ACGACGGCAA	GCTCCATGAT	GCGCGAAGGG	ATGAATGCGT	TGTCCGGTAG	TATTTCCCAG	540
AGCGCGCTTC	AGTTGGGGAT	CACTGGCGTG	GGCGCCAAAC	TGGAATATAA	GGGGCTGCAG	600
AATGAAAGAG	GCGCGCTTAA	ACATAATGCC	GCGAAGATCG	ATAAACTGAC	CACTGAAAGC	660
CACAGTATTA	AAAACGTGCT	GAACGGGCAG	AATAGCGTCA	AACTCGGTGC	TGAAGGCGTC	720
GATTCTCTGA	AATCGTTAAA	TATGAAGAAA	ACCGGTACCG	ATGCGACGAA	AAATCTTAAT	780
GATGCGACGC	TTAAATCTAA	TGCCGGAACC	AGCGCCACGG	AAAGTCTGGG	TATTAAAGAC	840
AGTAATAAAC	AAATCTCCCC	TGAACATCAG	GCTATTCTGT	CGAAACGTCT	TGAGTCTGTC	900
GAATCCGATA	TTCGTCTTGA	GCAGAATACC	ATGGATATGA	CCCGAATCGA	TGCGCGCAAG	960
ATGCAGATGA	CGGGCGATCT	GATTATGAAG	AACTCGGTCA	CGGTCCGGTG	TATTGCAGGG	1020
GCGTCCGGGC	AGTACGCCGC	TACTCAGGAA	CGTTCGAGC	AGCAAATTAG	CCAGGTGAAT	1080
AACCGGGTTG	CCAGCACCGC	ATCGGACGAA	GCCCGTGAAA	GTTACAGTAA	ATCGACCAGC	1140
CTGATTACAG	AAATGCTGAA	AACAATGGAG	AGCATTAACC	AGTCGAAAGC	ATCCGCACTC	1200
GCTGCTATCG	CAGGCAATAT	TCGCGCTTAA				1230

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCTTAATA	TTCAAAATTA	TTCCGCTTCT	CCTCATCCGG	GGATCGTTGC	CGAACGGCCG	60
CAGACTCCCT	CGGCGAGCGA	GCACGTCGAG	ACTGCCGTGG	TACCGTCTAC	CACAGAACAT	120
CGCGGTACAG	ATATCATTTT	ATTATCGCAG	GCGGCTACTA	AAATCCACCA	GGCACAGCAG	180

ACGCTGCAGT	CAACGCCACC	GATCTCTGAA	GAGAATAATG	ACGAGCGCAC	GCTGGCGCGC	240
CAGCAGTTGA	CCAGCAGCCT	GAATGCGCTG	GCGAAGTCCG	GCGTGTCTATT	ATCCGCAGAA	300
CAAAATGAGA	ACCTGCGGAG	CGCGTTTTCT	GCGCCGACGT	CGGCCTTATT	TAGCGCTTCG	360
CCTATGGCGC	AGCCGAGAAC	AACCATTTCT	GATGCTGAGA	TTTGGGATAT	GGTTTCCCAA	420
AATATATCGG	CGATAGGTGA	CAGCTATCTG	GGCGTTTATG	AAAACGTTGT	CGCAGTCTAT	480
ACCGATTTTT	ATCAGGCCTT	CAGTGATATT	CTTTCCAAAA	TGGGAGGCTG	GTTATTACCA	540
GGTAAGGACG	GTAATACCGT	TAAGCTAGAT	GTTACCTCAC	TCAAAAATGA	TTTAAACAGT	600
TTAGTCAATA	AATATAATCA	AATAAACAGT	AATACCGTTT	TATTTCCAGC	GCAGTCAGGC	660
AGCGGCGTTA	AAGTAGCCAC	TGAAGCGGAA	GCGAGACAGT	GGCTCAGTGA	ATTGAATTTA	720
CCGAATAGCT	GCCTGAAATC	TTATGGATCC	GGTTATGTCG	TCACCGTTGA	TCTGACGCCA	780
TTACAAAAAA	TGGTTCAGGA	TATTGATGGT	TTAGGCGCGC	CGGGAAAAGA	CTCAAACTC	840
GAAATGGATA	ACGCCAAATA	TCAAGCCTGG	CAGTCGGGTT	TTAAAGCGCA	GGAAGAAAAT	900
ATGAAAACCA	CATTACAGAC	GCTGACGCAA	AAATATAGCA	ATGCCAATTC	ATTGTACGAC	960
AACCTGGTAA	AAGTGCTGAG	CAGTACGATA	AGTAGCAGCC	TGGAAACCGC	CAAAAGCTTC	1020
CTGCAAGGAT	AA					1032

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGGTTACAA	GTGTAAGGAC	TCAGCCCCCC	GTCATAATGC	CAGGTATGCA	GACCGAGATC	60
AAAACGCAGG	CCACGAATCT	TGCGGCGAAT	CTTTCCGCAG	TCAGAGAAAG	TGCCACAGCG	120
ACGCTGTCAG	GGGAAATTAA	AGGCCCGCAA	CTGGAAGATT	TTCCCGCGCT	GATCAAACAG	180
CGGAGTCTGG	ATGC					194

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg	Lys	Ala	Glu	Glu	Thr	Asn	Arg	Ile	Met	Gly	Cys	Ile	Gly	Lys	Val
1				5					10					15	
Leu	Gly	Ala	Leu	Leu	Thr	Ile	Val	Ser	Val	Val	Ala	Ala	Val	Phe	Thr
			20					25					30		
Gly	Gly	Ala	Ser	Leu	Ala	Leu	Ala	Ala	Val	Gly	Leu	Ala	Val	Met	Val
		35					40					45			
Ala	Asp	Glu	Ile	Val	Lys	Ala	Ala	Thr	Gly	Val	Ser	Phe	Ile	Gln	Gln
	50					55					60				
Ala	Leu	Asn	Pro	Ile	Met	Glu	His	Val	Leu	Lys	Pro	Leu	Met	Glu	Leu
	65				70					75				80	
Ile	Gly	Lys	Ala	Ile	Thr	Lys	Ala	Leu	Glu	Gly	Leu	Gly	Val	Asp	Arg
			85					90					95		
Lys	Arg	Gln	Arg	Trp	Pro	Ala	Ala	Leu	Val	Arg	Leu	Ser	Pro	Leu	
		100					105					110			
Cys	His	Gly	Asp	Ala	Val	Ile	Val	Val	Ala	Val	Val	Gly	Lys	Gly	
		115					120				125				
Ala	Ala	Ala	Lys	Leu	Gly	Asn	Ala	Leu	Ser	Lys	Met	Met	Gly	Glu	Thr
	130					135					140				

Ile	Lys	Lys	Leu	Val	Pro	Asn	Val	Leu	Lys	Gln	Leu	Ala	Gln	Asn	Gly
145					150					155					160
Ser	Lys	Leu	Phe	Thr	Gln	Gly	Met	Gln	Arg	Ile	Thr	Ser	Gly	Leu	Gly
				165					170						175
Asn	Val	Gly	Ser	Lys	Met	Gly	Leu	Gln	Thr	Asn	Ala	Leu	Ser	Lys	Glu
				180					185					190	
Leu	Val	Gly	Asn	Thr	Leu	Asn	Lys	Val	Ala	Leu	Gly	Met	Glu	Val	Thr
				195			200					205			
Asn	Thr	Ala	Ala	Gln	Ser	Ala	Gly	Gly	Val	Ala	Glu	Gly	Val	Phe	Ile
	210					215					220				
Lys	Asn	Ala	Ser	Glu	Ala	Leu	Ala	Asp	Phe	Met	Leu	Ala	Arg	Phe	Ala
225					230					235					240
Met	Asp	Gln	Ile	Gln	Gln	Trp	Leu	Lys	Gln	Ser	Val	Glu	Ile	Phe	Gly
				245					250					255	
Glu	Asn	Gln	Lys	Val	Thr	Ala	Glu	Leu	Gln	Lys	Ala	Met	Ser	Ser	Ala
			260				265						270		
Val	Gln	Gln	Asn	Ala	Asp	Ala	Ser	Arg	Phe	Ile	Leu	Arg	Gln	Ser	Arg
		275					280						285		
Ala	Glx														
290															

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Leu	Ile	Ser	Asn	Val	Gly	Ile	Asn	Pro	Ala	Ala	Tyr	Leu	Asn	Asn
1				5					10					15	
His	Ser	Val	Glu	Asn	Ser	Ser	Gln	Thr	Ala	Ser	Gln	Ser	Val	Ser	Ala
			20					25					30		
Lys	Asp	Ile	Leu	Asn	Ser	Ile	Gly	Ile	Ser	Ser	Ser	Lys	Val	Ser	Asp
			35				40					45			
Leu	Gly	Leu	Ser	Pro	Thr	Leu	Ser	Ala	Pro	Ala	Pro	Gly	Val	Leu	Thr
	50					55					60				
Gln	Thr	Pro	Gly	Thr	Ile	Thr	Ser	Phe	Leu	Lys	Ala	Ser	Ile	Gln	Asn
	65				70					75					80
Thr	Asp	Met	Asn	Gln	Asp	Leu	Asn	Ala	Leu	Ala	Asn	Asn	Val	Thr	Thr
			85					90						95	
Lys	Ala	Asn	Glu	Val	Val	Gln	Thr	Gln	Leu	Arg	Glu	Gln	Gln	Ala	Glu
		100						105					110		
Val	Gly	Lys	Phe	Phe	Asp	Ile	Ser	Gly	Met	Ser	Ser	Ser	Ala	Val	Ala
		115					120					125			
Leu	Leu	Ala	Ala	Ala	Asn	Thr	Leu	Met	Leu	Thr	Leu	Asn	Gln	Ala	Asp
	130					135					140				
Ser	Lys	Leu	Ser	Gly	Lys	Leu	Ser	Leu	Val	Ser	Phe	Asp	Ala	Ala	Lys
145					150					155					160
Thr	Thr	Ala	Ser	Ser	Met	Met	Arg	Glu	Gly	Met	Asn	Ala	Leu	Ser	Gly
				165					170					175	
Ser	Ile	Ser	Gln	Ser	Ala	Leu	Gln	Leu	Gly	Ile	Thr	Gly	Val	Gly	Ala
			180					185					190		
Lys	Leu	Glu	Tyr	Lys	Gly	Leu	Gln	Asn	Glu	Arg	Gly	Ala	Leu	Lys	His
		195					200					205			
Asn	Ala	Ala	Lys	Ile	Asp	Lys	Leu	Thr	Thr	Glu	Ser	His	Ser	Ile	Lys
	210					215					220				
Asn	Val	Leu	Asn	Gly	Gln	Asn	Ser	Val	Lys	Leu	Gly	Ala	Glu	Gly	Val
225					230					235					240

Asp	Ser	Leu	Lys	Ser	Leu	Asn	Met	Lys	Lys	Thr	Gly	Thr	Asp	Ala	Thr
				245					250					255	
Lys	Asn	Leu	Asn	Asp	Ala	Thr	Leu	Lys	Ser	Asn	Ala	Gly	Thr	Ser	Ala
			260					265					270		
Thr	Glu	Ser	Leu	Gly	Ile	Lys	Asp	Ser	Asn	Lys	Gln	Ile	Ser	Pro	Glu
		275					280					285			
His	Gln	Ala	Ile	Leu	Ser	Lys	Arg	Leu	Glu	Ser	Val	Glu	Ser	Asp	Ile
	290					295					300				
Arg	Leu	Glu	Gln	Asn	Thr	Met	Asp	Met	Thr	Arg	Ile	Asp	Ala	Arg	Lys
305					310					315					320
Met	Gln	Met	Thr	Gly	Asp	Leu	Ile	Met	Lys	Asn	Ser	Val	Thr	Val	Gly
				325					330					335	
Gly	Ile	Ala	Gly	Ala	Ser	Gly	Gln	Tyr	Ala	Ala	Thr	Gln	Glu	Arg	Ser
			340					345					350		
Glu	Gln	Gln	Ile	Ser	Gln	Val	Asn	Asn	Arg	Val	Ala	Ser	Thr	Ala	Ser
		355					360					365			
Asp	Glu	Ala	Arg	Glu	Ser	Ser	Arg	Lys	Ser	Thr	Ser	Leu	Ile	Gln	Glu
	370					375					380				
Met	Leu	Lys	Thr	Met	Glu	Ser	Ile	Asn	Gln	Ser	Lys	Ala	Ser	Ala	Leu
385					390					395					400
Ala	Ala	Ile	Ala	Gly	Asn	Ile	Arg	Ala	Glx						
				405					410						

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Leu	Asn	Ile	Gln	Asn	Tyr	Ser	Ala	Ser	Pro	His	Pro	Gly	Ile	Val
1				5					10					15	
Ala	Glu	Arg	Pro	Gln	Thr	Pro	Ser	Ala	Ser	Glu	His	Val	Glu	Thr	Ala
			20					25					30		
Val	Val	Pro	Ser	Thr	Thr	Glu	His	Arg	Gly	Thr	Asp	Ile	Ile	Ser	Leu
		35					40					45			
Ser	Gln	Ala	Ala	Thr	Lys	Ile	His	Gln	Ala	Gln	Gln	Thr	Leu	Gln	Ser
	50					55					60				
Thr	Pro	Pro	Ile	Ser	Glu	Glu	Asn	Asn	Asp	Glu	Arg	Thr	Leu	Ala	Arg
65					70					75					80
Gln	Gln	Leu	Thr	Ser	Ser	Leu	Asn	Ala	Leu	Ala	Lys	Ser	Gly	Val	Ser
				85					90					95	
Leu	Ser	Ala	Glu	Gln	Asn	Glu	Asn	Leu	Arg	Ser	Ala	Phe	Ser	Ala	Pro
		100						105					110		
Thr	Ser	Ala	Leu	Phe	Ser	Ala	Ser	Pro	Met	Ala	Gln	Pro	Arg	Thr	Thr
		115					120					125			
Ile	Ser	Asp	Ala	Glu	Ile	Trp	Asp	Met	Val	Ser	Gln	Asn	Ile	Ser	Ala
	130					135					140				
Ile	Gly	Asp	Ser	Tyr	Leu	Gly	Val	Tyr	Glu	Asn	Val	Val	Ala	Val	Tyr
145					150					155					160
Thr	Asp	Phe	Tyr	Gln	Ala	Phe	Ser	Asp	Ile	Leu	Ser	Lys	Met	Gly	Gly
				165					170					175	
Trp	Leu	Leu	Pro	Gly	Lys	Asp	Gly	Asn	Thr	Val	Lys	Leu	Asp	Val	Thr
			180					185					190		
Ser	Leu	Lys	Asn	Asp	Leu	Asn	Ser	Leu	Val	Asn	Lys	Tyr	Asn	Gln	Ile
		195					200					205			
Asn	Ser	Asn	Thr	Val	Leu	Phe	Pro	Ala	Gln	Ser	Gly	Ser	Gly	Val	Lys
	210					215					220				

Val Ala Thr Glu Ala Glu Ala Arg Gln Trp Leu Ser Glu Leu Asn Leu
 225 230 235 240
 Pro Asn Ser Cys Leu Lys Ser Tyr Gly Ser Gly Tyr Val Val Thr Val
 245 250 255
 Asp Leu Thr Pro Leu Gln Lys Met Val Gln Asp Ile Asp Gly Leu Gly
 260 265 270
 Ala Pro Gly Lys Asp Ser Lys Leu Glu Met Asp Asn Ala Lys Tyr Gln
 275 280 285
 Ala Trp Gln Ser Gly Phe Lys Ala Gln Glu Glu Asn Met Lys Thr Thr
 290 295 300
 Leu Gln Thr Leu Thr Gln Lys Tyr Ser Asn Ala Asn Ser Leu Tyr Asp
 305 310 315 320
 Asn Leu Val Lys Val Leu Ser Ser Thr Ile Ser Ser Ser Leu Glu Thr
 325 330 335
 Ala Lys Ser Phe Leu Gln Gly Glx
 340

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Val Thr Ser Val Arg Thr Gln Pro Pro Val Ile Met Pro Gly Met
 1 5 10 15
 Gln Thr Glu Ile Lys Thr Gln Ala Thr Asn Leu Ala Ala Asn Leu Ser
 20 25 30
 Ala Val Arg Glu Ser Ala Thr Ala Thr Leu Ser Gly Glu Ile Lys Gly
 35 40 45
 Pro Gln Leu Glu Asp Phe Pro Ala Leu Ile Lys Gln Ala Ser Leu Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGCATTATT TTTTATCAT CGTAATCTGG TTGCTTAGCA TAAATACGGC ATGGGCTGAT 60
 TCTGGCTTCA GGCTGAAAAA ATGTTCAATA TTGAATCCGA ACTACTTTAC GCTATCGCCC 120
 AGCAGGAATC GCGATGAAA CCTGGCGCCA TTGGTCATAA CCGAGATGGT TCAACCGATC 180
 TTGGCCTGAT GCAAATTAAC AGCTTCCATA TGAAAAGGCT GAAAAAATG GGGATTAGTG 240
 AAAACAGTT GTTACAGGAC CCCTGCATTT CTGTCATTGT GGGCGACCTC CATTATATCA 300
 GATATGATGA AAATCTACGG TTATAGCTGG GAGGCCGTTG GCGCTTATAA TGCCGGGACG 360
 TCGCCGAAAC GATCGGATAT AAGGAAACGT TATGCTAAAA AAATTTGGGA GAATTACAGA 420
 AAATTAAAG GAATGTCAGC AGAAGAGAAA AACAAAAGAC TTTCTATCGC GGCAACAAA 480
 TAA 483

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGCTTGC	CGTCGTCATA	AGCAACTGGG	CTTGCATTGC	TTTtagTTGT	ACAAACTGTG	60
CAGGCGTCTT	CCAGCATTCT	ATTGTTCCGT	GAATCCGGAA	ATCTGCACGT	ACCTGCTCCA	120
GATTACTATG	AGGATTATCC	TTAAGTACAA	GGGCCGCCGC	CATCGTTCCG	GTTCTTCCCA	180
CTCCGCCCCAG	ACAATGAATC	ATCGGTAAAT	GCTTATCTGA	TGAACTACGC	CCCGGCCGCGC	240
CATTTTGGTT	ACTATTTTTC	ACCCTATCCG	CCAGGTATTC	TAACTGATCC	GTAGACGGTA	300
ACGGCTGGTG	ATCTGGCCAA	TTTTTCACAT	GCAATACCGG	GATTGTATAC	CGCTTTCCCC	360
GCAGGACAGT	TGCATATTGT	ATTGGTCTAT	CGCTTCTCCC	TGACTGGCTG	AGCTCTCTTT	420
TTGGCTGTTG	GTATGCACCT	CGCCAAAGGT	GTAGCTCCCT	CTGAAATAGG	TGGTAATTGT	480
TTTGCTTGCA	TCTGATCTTC	CGACGTTAAC	ACCACCAGGC	ACGAGCATTG	TTTTTCAAGA	540
AGCATTTTCA	TATGCGCTTC	CAGCGCATCC	CGGCGATTT			579

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	His	Tyr	Phe	Phe	Ile	Ile	Val	Ile	Trp	Leu	Leu	Ser	Ile	Asn	Thr	
1				5					10					15		
Ala	Trp	Ala	Asp	Ser	Gly	Phe	Arg	Leu	Lys	Lys	Cys	Ser	Ile	Leu	Asn	
			20					25					30			
Pro	Asn	Tyr	Phe	Thr	Leu	Ser	Pro	Ser	Arg	Asn	Arg	Arg	Glx	Asn	Leu	
		35					40					45				
Ala	Pro	Leu	Val	Ile	Thr	Glu	Met	Val	Gln	Pro	Ile	Leu	Ala	Glx	Cys	
	50					55				60						
Lys	Leu	Thr	Ala	Ser	Ile	Glx	Lys	Gly	Glx	Lys	Lys	Trp	Gly	Leu	Val	
	65				70				75					80		
Lys	Asn	Ser	Cys	Tyr	Arg	Thr	Pro	Ala	Phe	Leu	Ser	Leu	Trp	Ala	Thr	
			85					90						95		
Ser	Ile	Leu	Ser	Asp	Met	Met	Lys	Ile	Tyr	Gly	Tyr	Ser	Trp	Glu	Ala	
	100						105						110			
Val	Gly	Ala	Tyr	Asn	Ala	Gly	Thr	Ser	Pro	Lys	Arg	Ser	Asp	Ile	Arg	
	115					120					125					
Lys	Arg	Tyr	Ala	Lys	Lys	Ile	Trp	Glu	Asn	Tyr	Arg	Lys	Leu	Lys	Gly	
	130					135				140						
Met	Ser	Ala	Glu	Glu	Lys	Asn	Lys	Arg	Leu	Ser	Ile	Ala	Ala	Asn	Lys	
145					150				155					160		

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Trp	Pro	Gly	Thr	Ile	Cys	Gly	Gln	Gln	His	Ser	Ile	Asn	Gln	Gln	Thr
1				5					10					15	
Gln	Val	Lys	Leu	Ser	Asp	Gly	Met	Pro	Val	Pro	Val	Ile	Arg	Leu	Thr
			20					25					30		
Phe	Asp	Gly	Lys	Pro	Val	Ala	Leu	Ala	Gly	Ile	Arg	Thr	Gln	Lys	Ile
		35					40					45			
Arg	Pro	Asp	Arg	Leu	Glu	Ala	His	Met	Lys	Met	Leu	Leu	Glu	Lys	Glu
	50					55					60				
Cys	Ser	Cys	Leu	Val	Val	Leu	Thr	Ser	Glu	Arg	Ser	Asp	Ala	Gly	Lys
65				70					75					80	
Thr	Ile	Thr	Thr	Tyr	Phe	Arg	Gly	Ser	Tyr	Thr	Phe	Gly	Glu	Val	His
			85					90						95	
Thr	Asn	Ser	Gln	Lys	Val	Ser	Ser	Ala	Ser	Gln	Gly	Glu	Ala	Ile	Asp
			100					105					110		
Gln	Tyr	Asn	Met	Gln	Leu	Ser	Cys	Gly	Glu	Lys	Arg	Tyr	Thr	Ile	Pro
	115						120					125			
Val	Leu	His	Val	Lys	Asn	Trp	Pro	Asp	His	Gln	Pro	Leu	Pro	Ser	Thr
	130					135					140				
Asp	Gln	Leu	Glu	Tyr	Leu	Ala	Asp	Arg	Val	Lys	Asn	Ser	Asn	Gln	Asn
145					150					155					160
Gly	Ala	Pro	Gly	Arg	Ser	Ser	Ser	Asp	Lys	His	Leu	Pro	Met	Ile	His
			165					170						175	
Cys	Leu	Gly	Gly	Val	Gly	Arg	Thr	Gly	Thr	Met	Ala	Ala	Ala	Leu	Val
			180					185					190		
Leu	Lys	Asp	Asn	Pro	His	Ser	Asn	Leu	Glu	Gln	Val	Arg	Ala	Asp	Phe
	195						200					205			
Arg	Ile	His	Gly	Thr	Ile	Glu	Cys	Trp	Lys	Thr	Pro	Ala	Gln	Phe	Val
	210					215					220				
Gln	Leu	Lys	Ala	Met	Gln	Ala	Gln	Leu	Leu	Met	Thr	Thr	Ala	Ser	
225					230					235					

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCGTGATT	GCCTGAATAA	CGGCAATCCA	GTGCTTAACG	TGGGAGCGTC	AGGTCTTACC	60
ACCTTACCAG	ACCGTTTACC	ACCGCATATT	ACAACACTGG	TTATTCCTGA	TAATAATCTG	120
ACCAGCCTGC	CGGAGTTGCC	GGAAGGACTA	CGGGAGCTGG	AGGTCTCTGG	TAACCTACAA	180
CTGACCAGCC	TGCCATCGCT	GCCGCAGGGA	CTACAGAAGC	TGTGGGCCTA	TAATAATTGG	240
CTGGCCAGCC	TGCCGACGTT	GCCGCCAGGA	CTAGGGGATC	TGGCGGTCTC	TAATAACCAG	300
CTGACCAGCC	TGCCGAGATG	GCCGCCAGCA	CTACGGGAGC	TGAGGGTCTC	TGGTAACAAC	360
CTGACCAGCT	GCGCGCGCTG	CCGTCAGGAC	TACAGAAGCT	GTGGGCCTAT	AATAATCGGC	420
TGACCAGCCT	GCCGGAGATG	TCGCCAGGAC	TACAGGAGCT	GGATGTCTCT	CATAACCAGC	480
TGACCCGCCT	GCCGCAAAGC	CTCACGGGTC	TGTCTTCAGC	GGCACGCGTA	TATCTGGACG	540
GGAATCCACT	GTCTGTACGC	ACTCGTGACA	GGCTCTGCGG	ACATCATTGG	CCATTCAAGC	600
ATCAGGATAC	ACTTCGATAT	GGCGGGGCCT	TCCGTCCCCG	GGAAGCCCGG	GCACTGCACC	660
TGGCGGTGCG	TGACTGGCTG	ACGTCTGCAC	GGGAGGGGGA	AGCGGGCCAG	GCAGACAGAT	720
GGCAGGCGTT	CGGACTGGAA	GATAACGCCG	CCGCCTTCAG	CCTGGTCCTG	GACAGACTGC	780
GTGAGACGGA	AAACTTCAAA	AAAGACGCGG	GCTTTAAGGC	ACAGATATCA	TCCTGGCTGA	840
CACAACTGGC	TGAAGATGCT	GCGCTGAGAG	CAAAAACCTT	TGCCATGGCA	ACAGAGGCAA	900

CATCAACCTG	CGAGGACCGG	GTCACACATG	CCCTGCACCA	GATGAATAAC	GTACAACTGG	960
TACATAATGC	AGAAAAAGGG	GAATACGACA	ACAATCTCCA	GGGGCTGGTT	TCCACGGGGC	1020
GTGAGATGTT	CCGCCTGGCA	ACACTGGAAC	AGATTGCCCC	GGAAAAAGCC	GGAACACTGG	1080
CTTTAGTCGA	TGACGTTGAG	GTCTATCTGG	CGTTCCAGAA	TAAGCTGAAG	GAATCACTTG	1140
AGCTGACCAG	CGTGACGTCA	GAAATGCGTT	TCTTTGACGT	TTCCGGCGTG	ACGGTTTCAG	1200
ACCTTCAGGC	TGCGGACGTT	CAGGTGAAAA	CCGCTGAAAA	CAGCGGGTTC	AGTAAATGGA	1260
TACTGCAGTG	GGGGCCGTTA	CACAGCGTGC	TGGAACGCAA	AGTGCCGGAA	CGCTTTAACG	1320
CGCTTCGTGA	AAAGCAAATA	TCGATTATG	AAGACACGTA	CCGGAAGCTG	TATGACGAAG	1380
TGCTGAAATC	GTCCGGGCTG	GTCGACGATA	CCGATGCAGA	ACGTACTATC	GGAGTAAGTG	1440
CGATGGATAG	TGCGAAAAAA	GAATTTCTGG	ATGGCCTGCG	CGCTCTTG TG	GATGAGGTGC	1500
TGGGTAGCTA	TCTGACAGCC	CGGTGGCGTC	TTAACTGA			1538

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Arg	Asp	Cys	Leu	Asn	Asn	Gly	Asn	Pro	Val	Leu	Asn	Val	Gly	Ala
1				5				10						15	
Ser	Gly	Leu	Thr	Leu	Pro	Asp	Arg	Leu	Pro	Pro	His	Ile	Thr	Thr	
			20				25					30			
Leu	Val	Ile	Pro	Asp	Asn	Asn	Leu	Thr	Ser	Leu	Pro	Glu	Leu	Pro	Glu
		35					40				45				
Gly	Leu	Arg	Glu	Leu	Glu	Val	Ser	Gly	Asn	Leu	Gln	Leu	Thr	Ser	Leu
	50				55				60						
Pro	Ser	Leu	Pro	Gln	Gly	Leu	Gln	Lys	Leu	Trp	Ala	Tyr	Asn	Asn	Trp
	65			70					75					80	
Leu	Ala	Ser	Leu	Pro	Thr	Leu	Pro	Pro	Gly	Leu	Gly	Asp	Leu	Ala	Val
			85					90						95	
Ser	Asn	Asn	Gln	Leu	Thr	Ser	Leu	Pro	Glu	Met	Pro	Pro	Ala	Leu	Arg
			100				105						110		
Glu	Leu	Arg	Val	Ser	Gly	Asn	Asn	Leu	Thr	Ser	Leu	Arg	Ala	Leu	Pro
	115					120						125			
Ser	Gly	Leu	Gln	Lys	Leu	Trp	Ala	Tyr	Asn	Asn	Arg	Leu	Thr	Ser	Leu
	130				135						140				
Pro	Glu	Met	Ser	Pro	Gly	Leu	Gln	Glu	Leu	Asp	Val	Ser	His	Asn	Gln
	145				150				155					160	
Leu	Thr	Arg	Leu	Pro	Gln	Ser	Leu	Thr	Gly	Leu	Ser	Ser	Ala	Ala	Arg
			165					170						175	
Val	Tyr	Leu	Asp	Gly	Asn	Pro	Leu	Ser	Val	Arg	Thr	Arg	Asp	Arg	Leu
		180					185						190		
Cys	Gly	His	His	Trp	Pro	Phe	Arg	His	Gln	Asp	Thr	Leu	Arg	Tyr	Gly
		195				200					205				
Gly	Ala	Phe	Arg	Pro	Arg	Glu	Ala	Arg	Ala	Leu	His	Leu	Ala	Val	Ala
	210				215						220				
Asp	Trp	Leu	Thr	Ser	Ala	Arg	Glu	Gly	Glu	Ala	Ala	Gln	Ala	Asp	Arg
	225			230					235					240	
Trp	Gln	Ala	Phe	Gly	Leu	Glu	Asp	Asn	Ala	Ala	Ala	Phe	Ser	Leu	Val
			245					250						255	
Leu	Asp	Arg	Leu	Arg	Glu	Thr	Glu	Asn	Phe	Lys	Lys	Asp	Ala	Gly	Phe
		260					265						270		
Lys	Ala	Gln	Ile	Ser	Ser	Trp	Leu	Thr	Gln	Leu	Ala	Glu	Asp	Ala	Ala
		275				280						285			
Leu	Arg	Ala	Lys	Thr	Phe	Ala	Met	Ala	Thr	Glu	Ala	Thr	Ser	Thr	Cys
	290					295					300				

Glu Asp Arg Val Thr His Ala Leu His Gln Met Asn Asn Val Gln Leu
 305 310 315 320
 Val His Asn Ala Glu Lys Gly Glu Tyr Asp Asn Asn Leu Gln Gly Leu
 325 330 335
 Val Ser Thr Gly Arg Glu Met Phe Arg Leu Ala Thr Leu Glu Gln Ile
 340 345 350
 Ala Arg Glu Lys Ala Gly Thr Leu Ala Leu Val Asp Asp Val Glu Val
 355 360 365
 Tyr Leu Ala Phe Gln Asn Lys Leu Lys Glu Ser Leu Glu Leu Thr Ser
 370 375 380
 Val Thr Ser Glu Met Arg Phe Phe Asp Val Ser Gly Val Thr Val Ser
 385 390 395 400
 Asp Leu Gln Ala Ala Asp Val Gln Val Lys Thr Ala Glu Asn Ser Gly
 405 410 415
 Phe Ser Lys Trp Ile Leu Gln Trp Gly Pro Leu His Ser Val Leu Glu
 420 425 430
 Arg Lys Val Pro Glu Arg Phe Asn Ala Leu Arg Glu Lys Gln Ile Ser
 435 440 445
 Asp Tyr Glu Asp Thr Tyr Arg Lys Leu Tyr Asp Glu Val Leu Lys Ser
 450 455 460
 Ser Gly Leu Val Asp Asp Thr Asp Ala Glu Arg Thr Ile Gly Val Ser
 465 470 475 480
 Ala Met Asp Ser Ala Lys Lys Glu Phe Leu Asp Gly Leu Arg Ala Leu
 485 490 495
 Val Asp Glu Val Leu Gly Ser Tyr Leu Thr Ala Arg Trp Arg Leu Asn
 500 505 510
 Glx

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCAAAGCCG	AGGAAACGAA	CCGCATTATG	GGATGTATCG	GGAAAGTCCT	CGGCGCGCTG	60
CTAACCATTG	TCAGCGTTGT	GGCCGCTGTT	TTTACCGGTG	GGGCGAGTCT	GGCGCTGGCT	120
GCGGTGGGAC	TTGCGGTAAT	GGTGGCCGAT	GAAATTGTGA	AGGCGGCGAC	GGGAGTGTCT	180
TTTATTTCAGC	AGGCGCTAAA	CCCATTATG	GAGCATGTGC	TGAAGCCGTT	AATGGAGCTG	240
ATTGGCAAGG	CGATTACCAA	AGCGCTGGAA	GGATTAGGCG	TCGATAAGAA	AACGGCAGAG	300
ATGGCCGGCA	GCATTGTTGG	TGCGATTGTC	GCCGCTATTG	CCATGGTGGC	GGTCATTGTG	360
GTGGTCGCAG	TTGTCGGGAA	AGGCGCGGCG	GCGAACTGG	GTAACGCGCT	GAGCAAAATG	420
ATGGGCGAAA	CGATTAAGAA	GTTGGTGCCT	AACGTGCTGA	AACAGTTGGC	GCAAAACGGC	480
AGCAAACCTCT	TTACCCAGGG	GATGCAACGT	ATTACTAGCG	GTCTGGGTAA	TGTGGGTAGC	540
AAGATGGGCC	TGCAAACGAA	TGCCTTAAGT	AAAGAGCTGG	TAGGTAATAC	CCTAAATAAA	600
GTGGCGTTGG	GCATGGAAGT	CACGAATACC	GCAGCCCAGT	CAGCCGGTGG	TGTTGCCGAG	660
GGCGTATTTA	TTAAAAATGC	CAGCGAGGCG	CTTGCTGATT	TTATGCTCGC	CCGTTTTGCC	720
ATGGATCAGA	TTCAGCAGTG	GCTTAAACAA	TCCGTAGAAA	TATTTGGTGA	AAACCAGAAG	780
GTAACGGCGG	AACTGCAAAA	AGCCATGTCT	TCTGCGGTAC	AGCAAAATGC	GGATGCTTCG	840
CGTTTTATTTC	TGCGCCAGAG	TCGCGCATAA	AAACTGCCAA	AATAAAGGGA	GAAAAATATG	900
TTAATTAGTA	ATGTGGGAAT	AAATCCCGCC	GCTTATTTAA	ATAATCATTC	TGTTGAGAAT	960
AGTTTCACAGA	CAGCTTCGCA	ATCCGTTAGC	GCTAAAGATA	TTCTGAATAG	TATTGGTATT	1020
AGCAGCAGTA	AAGTCAGTGA	CCTGGGGTTG	AGTCCTACAC	TGAGCGCGCC	TGCGCCAGGG	1080
GTATTAACGC	AAACCCCGCG	AACGATCACG	TCCTTTTTAA	AAGCCAGTAT	TCAAAATACC	1140
GACATGAATC	AGGATTTGAA	TGCTCTGGCA	AATAATGTCA	CGACTAAAGC	GAATGAGGTT	1200
GTGCAAAACC	AGTTACGCGA	GCAGCAGGCA	GAAGTCGGAA	AGTTTTTTGA	TATTAGCGGA	1260

ATGTCTTCCA	GTGCCGTTGC	GCTGTTGGCT	GCCGCGAATA	CGTTAATGCT	GACGTTGAAC	1320
CAGGCTGATA	GCAAACGTGC	TGGTAAGTTG	TCATTAGTCA	GTTTTGATGC	AGCTAAAACG	1380
ACGGCAAGCT	CCATGATGCG	CGAAGGGATG	AATGCGTTGT	CCGGTAGTAT	TTCCCAGAGC	1440
GCGCTTCAGT	TGGGGATCAC	TGGCGTGGGC	GCCAAACTGG	AATATAAGGG	GCTGCAGAAT	1500
GAAAGAGGCG	CGCTTAAACA	TAATGCCGCG	AAGATCGATA	AACTGACCAC	TGAAAGCCAC	1560
AGTATTAAAA	ACGTGCTGAA	CGGGCAGAAT	AGCGTCAAAC	TCGGTGCTGA	AGGCGTCGAT	1620
TCTCTGAAAT	CGTTAAATAT	GAAGAAAACC	GGTACCGATG	CGACGAAAAA	TCTTAATGAT	1680
GCGACGCTTA	AATCTAATGC	CGGAACCAGC	GCCACGGAAA	GTCTGGGTAT	TAAAGACAGT	1740
AATAAACAAA	TCTCCCCTGA	ACATCAGGCT	ATTCTGTGCA	AACGTCTTGA	GTCTGTGCAA	1800
TCCGATATTC	GTCTTGAGCA	GAATACCATG	GATATGACCC	GAATCGATGC	GCGCAAGATG	1860
CAGATGACGG	GCGATCTGAT	TATGAAGAAC	TCGGTCACGG	TCGGTGGTAT	TGCAGGGGCG	1920
TCCGGGCAGT	ACGCCGCTAC	TCAGGAACGT	TCCGAGCAGC	AAATTAGCCA	GGTGAATAAC	1980
CGGGTTGCCA	GCACCGCATC	GGACGAAGCC	CGTGAAAGTT	CACGTAAATC	GACCAGCCTG	2040
ATTCAGGAAA	TGCTGAAAAC	AATGGAGAGC	ATTAACCATG	CGAAAGCATC	CGCACTCGCT	2100
GCTATCGCAG	GCAATATTCT	CGCTTAATCT	GAAAGGTCAT	CTATACGCCA	TCATGGGTGT	2160
GATTTAATCG	CGCTCCTGAT	GGCGAACTGG	GGATATTATG	CTTAATATTC	AAAATTATTC	2220
CGCTTCTCCT	CATCCGGGGA	TCGTTGCCGA	ACGGCCGCAG	ACTCCCTCGG	CGAGCGAGCA	2280
CGTCGAGACT	GCCGTGGTAC	CGTCTACCAC	AGAACATCGC	GGTACAGATA	TCATTTTCATT	2340
ATCGCAGGCG	GCTACTAAAA	TCCACCAGGC	ACAGCAGACG	CTGCAGTCAA	CGCCACCGAT	2400
CTCTGAAGAG	AATAATGACG	AGCGCACGCT	GGCGCGCCAG	CAGTTGACCA	GCAGCCTGAA	2460
TGCGCTGGCG	AAGTCCGGCG	TGTCATTATC	CGCAGAACAA	AATGAGAACC	TGCGGAGCGC	2520
GTTTTCTCGC	CCGACGTCGG	CCTTATTTAG	CGCTTCGCCT	ATGGCGCAGC	CGAGAACAAAC	2580
CATTTCTGAT	GCTGAGATTT	GGGATATGGT	TTCCCAAAAT	ATATCGGCGA	TAGGTGACAG	2640
CTATCTGGGC	GTTTATGAAA	ACGTTGTGCG	AGTCTATACC	GATTTTTTATC	AGGCCTTCAG	2700
TGATATTCTT	TCCAAAATGG	GAGGCTGGTT	ATTACCAGGT	AAGGACGGTA	ATACCGTTAA	2760
GCTAGATGTT	ACCTCACTCA	AAAATGATTT	AAACAGTTTA	GTCAATAAAT	ATAATCAAAT	2820
AAACAGTAAT	ACCGTTTTAT	TTCCAGCGCA	GTCAGGCAGC	GGCGTTAAAG	TAGCCACTGA	2880
AGCGGAAGCG	AGACAGTGGC	TCAGTGAATT	GAATTTACCG	AATAGCTGCC	TGAAATCTTA	2940
TGGATCCGGT	TATGTCGTCA	CCGTTGATCT	GACGCCATTA	CAAAAAATGG	TTCAGGATAT	3000
TGATGGTTTA	GGCGCGCCGG	GAAAAGACTC	AAAACCTCGA	ATGGATAACG	CCAAATATCA	3060
AGCCTGGCAG	TCGGGTTTTA	AAGCGCAGGA	AGAAAATATG	AAAACCACAT	TACAGACGCT	3120
GACGCAAAAA	TATAGCAATG	CCAATTCAAT	GTACGACAAC	CTGGTAAAAG	TGCTGAGCAG	3180
TACGATAAGT	AGCAGCCTGG	AAACCGCCAA	AAGCTTCCTG	CAAGGATAAC	AGAAGAGGAT	3240
ATTAATAATG	GTTACAAGTG	TAAGGACTCA	GCCCCCGTGC	ATAATGCCAG	GTATGCAGAC	3300
CGAGATCAAA	ACGCAGGCCA	CGAATCTTGC	GGCGAATCTT	TCCGCAGTCA	GAGAAAGTGC	3360
CACAGCGACG	CTGTCAAGGG	AAATTAAAGG	CCCGCAACTG	GAAGATTTTC	CCGCGCTGAT	3420
CAAACAGGCG	AGTCTGGATG	C				3441

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCTCAGCA	ACGTGTCGAA	AGCCTGTAAA	ATCATGGGCG	TCTCGCGCGA	TACGTTTTAC	60
CGTTATCGTG	AACTGGCCGA	TGAAGGCGGC	GTTGATGCGC	TGATAAATCG	TAGTCGCCGC	120
GTACCTAACC	TTAAGAACCG	TACCGATGAG	GCAACTGAGC	AAGCTGTTGT	TGATTATGCC	180
GTTGCGTTCC	CGGCCCATGG	TCAGCACCGA	ACTGCGCAAA	CAGGACGTTT	TTATCTCCGG	240
TAGTGATGTC	CATTCCGTCT	GGCTGCGCAC	AACCTTGAGA	ACTTCAAAAA	ACGCCTGAAA	300
GCGCTGGAAG	AAAAAGTGGC	CCGCGATGGC	ATTGAACTGA	CTGCCAGATC	GCCGCGCTGG	360
AGCGTAAAGC	CAGTGATGAT	GAAGCCTGTG	GTGAGATTGA	AACCGTTCAT	CCGGGATATC	420
TGGGGTCACA	GGACACGTTT	TACGTGGGCA	ACCTGAAAGG	CGTTGGGCGA	ATCTATCAGC	480
AGACGTTTCG	TGATAAGTTC	TCGAAGGTGG	CTCACTGCAA	GCGCTATATC	ACCAAAACGC	540
CGATTACAGC	GGCTGATTTC	CTGAATGATC	GTGTACTGCC	GTTTATGAGT	CTCAGGGCCT	600
GCCGATGCTA	AGGATACTGA	CAGACAGGGG	TACAGAATAT	TGCGGCAAAG	TGGAACATCA	660
TGATTATCAG	CTTTATCTGG	AGATAAATGA	CATCGAACAC	ACGAAAACGA	AGGCGATGTC	720

CCCGCAGACC	AATGGCATCT	GCGAGCGGTT	CCATAAAACG	ATACTGAACG	AATTTTATCA	780
GGTGACGTTT	CGCAAAAAGT	TATATGGCGA	TTTTGATACA	TTACAATCGG	ATCTTGATGA	840
ATGGCTGGTT	CACTATAATA	ATGAGCGAAC	CCATCAGGGA	AAAATGTGCT	GTGGCCGGAC	900
GCCGATGGAA	ACGTTACTTG	ATGGAAAACG	CATCTGGTCT	GAGAAGAATT	TAAGCCAGAT	960
GTAATCTGAC	AGATACCTGT	ATAAATAACC	GGTAACTGTC	AGATCAGGTC	TGAGCTAATA	1020
CAACTAATTG	TATGTTATTT	GTCGTTTATT	GCTAAATATA	TATCGTTAAT	TGAAGGCTTG	1080
ATGCGTGTGT	CTGCGTTAAT	CTCTTTTCAT	TGTGCTGTAA	ATTAGGCAGT	GGAAATATGTT	1140
TAATATCCGC	AATACACAAC	CTTCTGTAAG	TATGCAGGCT	ATTGCTGGTG	CAGCGGCACC	1200
AGAGGCATCT	CCGGAAGAAA	TTGTATGGGA	AAAATTCAGG	TTTTTTTCCC	GCAGGAAAAT	1260
TACGAAGAAG	CGCAACAGTG	TCTCGCTGAA	CTTTGCCATC	CGGCCCCGGG	AATGTTGCCT	1320
GATCATATCA	GCAGCCAGTT	TGCGCGTTTA	AAAGCGCTTA	CCTTCCCCGC	GTGGGAGGAG	1380
AATATTCAGT	GTAACAGGGA	TGGTATAAAT	CAGTTTTGTA	TTCTGGATGC	AGGCAGCAAG	1440
GAGATATTGT	CAATCACTCT	TGATGATGCC	GGGAACATA	CCGTGAATTG	TCAGGGGTAC	1500
AGTGAAGCAC	ATGACTTCAT	CATGGACACA	GAACCGGGAG	AGGAATGCAC	AGAATTCGCG	1560
GAGGGGGCAT	CCGGGACATC	CCTCCGCCCT	GCCACAACGG	TTTCACAGAA	GGCAGCAGAG	1620
TATGATGCTG	TCTGGTCAAA	TGGGAAAAGG	ATGCACCAGC	AGGAGAGTCA	CCCGGCCGCG	1680
CAGCAGTGGT	ACAGGAAATG	CGTGATTGCC	TGAATAACGG	CAATCCAGTG	CTTAACGTGG	1740
GAGCGTCAGG	TCTTACCACC	TTACCAGACC	GTTTACCACC	GCATATTACA	ACACTGGTTA	1800
TTCTTGATAA	TAATCTGACC	AGCCTGCCGG	AGTTGCCGGA	AGGACTACGG	GAGCTGGAGG	1860
TCTCTGGTAA	CCTACAACCTG	ACCAGCCTGC	CATCGCTGCC	GCAGGGACTA	CAGAAGCTGT	1920
GGGCCTATAA	TAATTTGGCTG	GCCAGCCTGC	CGAGCTTGCC	GCCAGGACTA	GGGGATCTGG	1980
GGGTCTCTAA	TAACAGCTG	ACCAGCCTGC	CGGAGATGCC	GCCAGCACTA	CGGGAGCTGA	2040
GGGTCTCTGG	TAACAACCTG	ACCAGCTGCG	CGCGCTGCCG	TCAGGACTAC	AGAAGCTGTG	2100
GGCCTATAAT	AATCGGCTGA	CCAGCCTGCC	GGAGATGTGC	CCAGGACTAC	AGGAGCTGGA	2160
TGCGTGATTG	CCTGAATAAC	GGCAATCCAG	TGCTTAACGT	GGGAGCGTCA	GGTCTTACCA	2220
CCTTACCAGA	CCGTTTACCA	CCGCATATTA	CAACACTGGT	TATTCCTGAT	AATAATCTGA	2280
CCAGCCTGCC	GGAGTTGCCG	GAAGGACTAC	GGGAGCTGGA	GGTCTCTGGT	AACCTACAAC	2340
TGACCAGCCT	GCCATCGCTG	CCGCAGGGAC	ATCAGAAGCT	GTGGGCCTAT	AATAATTGGC	2400
TGGCCAGCCT	GCCGACGTTG	CCGCCAGGAC	TAGGGGATCT	GGCGGTCTCT	AATAACCAGC	2460
TGACCAGCCT	GCCGGAGATG	CCGCCAGCAC	TACGGGAGCT	GAGGGTCTCT	GGTAACAACC	2520
TGACCAGCTG	CGCGCGCTGC	CGTCAGGACT	ACAGAAGCTG	TGGGCCTATA	ATAATCGGCT	2580
GACCAGCCTG	CCGGAGATGT	CGCCAGGACT	ACAGGAGCTG	GATGTCTCTC	ATAACCAGCT	2640
GACCCGCCTG	CCGCAAAGCC	TCACGGGTCT	GTCTTCAGCG	GCACGCGTAT	ATCTGGACGG	2700
GAATCCACTG	TCTGTACGCA	CTCGTGACAG	GCTCTGCCGA	CATCATTGGC	CATTACGGCA	2760
TCAGGATACA	CTTCGATATG	GCGGGGCCTT	CCGTCCCCGG	GAAGCCCAGG	CACTGCACCT	2820
GGCGGTGCTG	GACTGGCTGA	CGTCTGCACG	GGAGGGGGAA	GCGGCCAGG	CAGACAGATG	2880
GCAGGCGTTC	GGACTGGAAG	ATAACGCCGC	CGCCTTCAGC	CTGGTCCTGG	ACAGACTGCG	2940
TGAGACGGAA	AACTTCAAAA	AAGACGCGGG	CTTTAAGGCA	CAGATATCAT	CCTGGCTGAC	3000
ACAACTGGCT	GAAGATGCTG	CGCTGAGAGC	AAAAACCTTT	GCCATGGCAA	CAGAGGCAAC	3060
ATCAACCTGC	GAGGACCGGG	TCACACATGC	CCTGCACCAG	ATGAATAACG	TACAACTGGT	3120
ACATAATGCA	GAAAAAGGGG	AATACGACAA	CAATCTCCAG	GGGCTGGTTT	CCACGGGGCG	3180
TGAGATGTTT	CGCCTGGCAA	CACTGGAACA	GATTGCCCGG	GAAAAAGCCG	GAACACTGGC	3240
TTTAGTCGAT	GACGTTGAGG	TCTATCTGGC	GTTCCAGAAT	AAGCTGAAGG	AATCACTTGA	3300
GCTGACCAGC	GTGACGTCAG	AAATGCGTTT	CTTTGACGTT	TCCGGCGTGA	CGGTTTCAGA	3360
CCTTCAGGCT	GCGGACGTTT	AGGTGAAAAC	CGCTGAAAAC	AGCGGGTTCA	GTAAATGGAT	3420
ACTGCAGTGG	GGGCCGTTAC	ACAGCGTGCT	GGAACGCAAA	GTGCCGGAAC	GCTTTAACGC	3480
GCTTCGTGAA	AAGCAAATAT	CGGATTATGA	AGACACGTAC	CGGAAGCTGT	ATGACGAAAGT	3540
GCTGAAATCG	TCCGGGCTGG	TCGACGATAC	CGATGCAGAA	CGTACTATCG	GAGTAAGTGC	3600
GATGGATAGT	GCGAAAAAAG	AATTTCTGGA	TGGCCTGCGC	GCTCTGTGGG	ATGAGGTGCT	3660
GGGTAGCTAT	CTGACAGCCC	GGTGGCGTCT	TAAGTGAGCA	CGATATTCTC	CGCACCAGGC	3720
GAATGTGGTG	CGGTGAACAA	AGATATTCTT	TGGACAAACA	ACATGAGACA	GCACTGATGA	3780
TGCACAGGTG	AAACAGGGGA	GACTTCTTCA	GTCAGGGCGT	ACGCAACTCA	ACCTTTTTCGA	3840
CGATACGCGC	C					3851

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCAGGTGGAT ACGGA 15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TAGCGTCCTC CCCATGTGCG 20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCGGCGCTAC TGGCGGCG 18

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCGTTTCAA CAGCCCCG 18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGGGGCTGTT GAAACGC 17

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AACCTGGCCT TTTCAG 16

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCAGGGAGC CTTGCTTGG 19

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGCCTGGCC AGTTCTCCA 19

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGGATCCA TTATGGGATG TATCGG 26

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCGGCAGCAA AATGTTGCAG

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Val Thr Ser Val Arg Thr Gln Pro Pro Val Ile Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Leu Ile Ser Asn Val Gly Ile Asn Pro Ala Ala Tyr Leu Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Asn Asn Leu Thr Leu Ser Xaa Phe Xaa Lys Val Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Leu Ile Ser Asn Val Gly Ile Asn Pro Ala Ala Tyr Leu Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Phe Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Thr Pro Trp Ser Gly Tyr Leu Asp Asp Val Ser Ala Lys Phe
1 5 10 15
Asp Thr Gly Val Asp Asn Leu Gln Thr Gln Val Thr Glu Ala Leu Asp
20 25 30
Lys Leu Ala Ala Lys Pro Ser Asp Pro Ala Leu Leu Ala Ala Tyr Gln
35 40 45
Ser Lys Leu Ser Glu Tyr Asn Leu Tyr Arg Asn Ala Gln Ser Asn Thr
50 55 60
Val Lys Val Phe Lys Asp Ile Asp Ala Ala Ile Ile Gln Asn Phe Arg
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ser Val Thr Val Pro Asn Asp Asp Trp Thr Leu Ser Ser Leu Ser
1 5 10 15
Glu Thr Phe Asp Asp Gly Thr Gln Thr Leu Gln Gly Glu Leu Thr Leu
20 25 30
Ala Leu Asp Lys Leu Ala Lys Asn Pro Ser Asn Pro Gln Leu Leu Ala
35 40 45
Glu Tyr Gln Ser Lys Leu Ser Glu Tyr Thr Leu Tyr Arg Asn Ala Gln
50 55 60

Ser Asn Thr Val Lys Val Ile Lys Asp Val Asp Ala Ala Ile Ile Gln
 65 70 75 80
 Asn Phe Arg

(2) INFORMATION FOR SEQ ID NO:34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ser Asn Phe Ser Gly Phe Thr Lys Gly Asn Asp Ile Ala Asp Leu
 1 5 10 15
 Asp Ala Val Ala Gln Thr Leu Lys Lys Pro Ala Asp Asp Ala Asn Lys
 20 25 30
 Ala Val Asn Asp Ser Ile Ala Ala Leu Lys Asp Thr Pro Asp Asn Pro
 35 40 45
 Ala Leu Leu Ala Asp Leu Gln His Ser Ile Asn Lys Trp Ser Val Ile
 50 55 60
 Tyr Asn Ile Ser Ser Thr Ile Val Arg Ser Met Lys Asp Leu Met Gln
 65 70 75 80
 Gly Ile Leu Gln Lys Phe Pro
 85

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Ser Ile Ala Thr Ile Val Pro Glu Asn Ala Val Ile Gly Gln Ala
 1 5 10 15
 Val Asn Ile Arg Ser Met Glu Thr Asp Ile Val Ser Leu Asp Asp Arg
 20 25 30
 Leu Leu Gln Ala Phe Ser Gly Ser Ala Ile Ala Thr Ala Val Asp Lys
 35 40 45
 Gln Thr Ile Thr Asn Arg Ile Glu Asp Pro Asn Leu Val Thr Asp Pro
 50 55 60
 Lys Glu Leu Ala Ile Ser Gln Glu Met Ile Ser Asp Tyr Asn Leu Tyr
 65 70 75 80
 Val Ser Met Val Ser Thr Leu Thr Arg Lys Gly Val Gly Ala Val Glu
 85 90 95
 Thr Leu Leu Arg Ser
 100

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Asn	Tyr	Ile	Tyr	Pro	Val	Asn	Gln	Val	Asp	Ile	Ile	Lys	Ala	Ser
1				5					10					15	
Asp	Phe	Gln	Ser	Gln	Glu	Ile	Ser	Ser	Leu	Glu	Asp	Val	Val	Ser	Ala
		20						25					30		
Lys	Tyr	Ser	Asp	Ile	Lys	Met	Asp	Thr	Asp	Ile	Gln	Val	Ser	Gln	Ile
		35					40					45			
Met	Glu	Met	Val	Ser	Asn	Pro	Glu	Ser	Leu	Asn	Pro	Glu	Ser	Leu	Ala
	50					55				60					
Lys	Leu	Gln	Thr	Thr	Leu	Ser	Asn	Tyr	Ser	Ile	Gly	Val	Ser	Leu	Ala
65					70					75					80
Gly	Thr	Leu	Ala	Arg	Lys	Thr	Val	Ser	Ala	Val	Glu	Thr	Leu	Leu	Lys
				85					90					95	
Ser															

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ile	Arg	Tyr	Lys	Gly	Phe	Ile	Leu	Phe	Leu	Leu	Leu	Met	Leu	Ile
1				5					10					15	
Gly	Cys	Glu	Gln	Arg	Glu	Glu	Leu	Ile	Ser	Asn	Leu	Ser	Gln	Arg	Gln
		20						25					30		
Ala	Asn	Glu	Ile	Ile	Ser	Val	Leu	Glu	Arg	His	Asn	Ile	Thr	Ala	Arg
		35					40					45			
Lys	Val	Asp	Gly	Gly	Lys	Gln	Gly	Ile	Ser	Val	Gln	Val	Glu	Lys	Gly
	50					55				60					
Thr	Phe	Ala	Ser	Ala	Val	Asp	Leu	Met	Arg	Met	Tyr	Asp	Leu	Pro	Asn
65					70					75					80
Pro	Glu	Arg	Val	Asp	Ile	Ser	Gln	Met	Phe	Pro	Thr	Asp	Ser	Leu	Val
				85					90					95	
Ser	Ser	Pro	Arg	Ala	Glu	Lys	Ala	Arg	Leu	Tyr	Ser	Ala	Ile	Glu	Gln
		100					105					110			
Arg	Leu	Glu	Gln	Ser	Leu	Val	Ser	Ile	Gly	Gly	Val	Ile	Ser	Ala	Lys
	115					120					125				
Ile	His	Val	Ser	Tyr	Asp	Leu	Glu	Glu	Lys	Asn	Ile	Ser	Ser	Lys	Pro
130					135					140					
Met	His	Ile	Ser	Val	Ile	Ala	Ile	Tyr	Asp	Ser	Pro	Lys	Glu	Ser	Glu
145					150					155					160
Leu	Leu	Val	Ser	Asn	Ile	Lys	Arg	Phe	Leu	Lys	Asn	Thr	Phe	Ser	Asp
			165						170					175	
Val	Lys	Tyr	Glu	Asn	Ile	Ser	Val	Ile	Leu	Thr	Pro	Lys	Glu	Glu	Tyr
		180						185					190		
Val	Tyr	Thr	Asn	Val	Gln	Pro	Val	Lys	Glu	Val	Lys	Ser	Glu	Phe	Leu
	195					200						205			
Thr	Asn	Glu	Val	Ile	Tyr	Leu	Phe	Leu	Gly	Met	Ala	Val	Leu	Val	Val
	210					215					220				
Ile	Leu	Leu	Val	Trp	Ala	Phe	Lys	Thr	Gly	Trp	Phe	Lys	Arg	Asn	Lys
225					230					235					240
Ile															

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Lys	Val	Lys	Thr	Ser	Leu	Ser	Thr	Leu	Ile	Leu	Ile	Leu	Phe	Leu
1				5					10					15	
Thr	Gly	Cys	Lys	Val	Asp	Leu	Tyr	Thr	Gly	Ile	Ser	Gln	Lys	Glu	Gly
			20					25					30		
Asn	Glu	Met	Leu	Ala	Leu	Leu	Arg	Gln	Glu	Gly	Leu	Ser	Ala	Asp	Lys
		35					40					45			
Glu	Pro	Asp	Lys	Asp	Gly	Lys	Ile	Lys	Leu	Leu	Val	Glu	Glu	Ser	Asp
	50					55					60				
Val	Ala	Gln	Ala	Ile	Asp	Ile	Leu	Lys	Arg	Lys	Gly	Tyr	Pro	His	Glu
	65				70					75				80	
Ser	Phe	Ser	Thr	Leu	Gln	Asp	Val	Phe	Pro	Lys	Asp	Gly	Leu	Ile	Ser
			85					90						95	
Ser	Pro	Ile	Glu	Glu	Leu	Ala	Arg	Leu	Asn	Tyr	Ala	Lys	Ala	Gln	Glu
			100					105					110		
Ile	Ser	Arg	Thr	Leu	Ser	Glu	Ile	Asp	Gly	Val	Leu	Val	Ala	Arg	Val
	115					120						125			
His	Val	Val	Leu	Pro	Glu	Glu	Gln	Asn	Asn	Lys	Gly	Lys	Lys	Gly	Val
	130					135					140				
Ala	Ala	Ser	Ala	Ser	Val	Phe	Ile	Lys	His	Ala	Ala	Asp	Ile	Gln	Phe
	145				150					155				160	
Asp	Thr	Tyr	Ile	Pro	Gln	Ile	Lys	Gln	Leu	Val	Asn	Asn	Ser	Ile	Glu
			165					170					175		
Gly	Leu	Ala	Tyr	Asp	Arg	Ile	Ser	Val	Ile	Leu	Val	Pro	Ser	Val	Asp
		180					185						190		
Val	Arg	Gln	Ser	Ser	His	Leu	Pro	Arg	Asn	Thr	Ser	Ile	Leu	Ser	Ile
	195						200					205			
Gln	Val	Ser	Glu	Glu	Ser	Lys	Gly	Arg	Leu	Ile	Gly	Leu	Leu	Ser	Leu
	210					215					220				
Leu	Ile	Leu	Leu	Leu	Pro	Val	Thr	Asn	Leu	Ala	Gln	Tyr	Phe	Trp	Leu
	225				230					235					240
Gln	Arg	Lys	Lys												

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Ile	Arg	Arg	Tyr	Leu	Tyr	Thr	Phe	Leu	Leu	Val	Met	Thr	Leu	Ala
1				5					10					15	
Gly	Cys	Lys	Asp	Lys	Asp	Leu	Leu	Lys	Gly	Leu	Asp	Gln	Glu	Gln	Ala
			20					25					30		
Asn	Glu	Val	Ile	Ala	Val	Leu	Gln	Met	His	Asn	Ile	Glu	Ala	Asn	Lys
		35					40					45			

Ile	Asp	Ser	Gly	Lys	Leu	Gly	Tyr	Ser	Ile	Thr	Val	Ala	Glu	Pro	Asp
50						55					60				
Phe	Thr	Ala	Ala	Val	Tyr	Trp	Ile	Lys	Thr	Tyr	Gln	Leu	Pro	Pro	Arg
65					70					75					80
Pro	Arg	Val	Glu	Ile	Ala	Gln	Met	Phe	Pro	Ala	Asp	Ser	Leu	Val	Ser
				85					90					95	
Ser	Pro	Arg	Ala	Glu	Lys	Ala	Arg	Leu	Tyr	Ser	Ala	Ile	Glu	Gln	Arg
			100					105					110		
Leu	Glu	Gln	Ser	Leu	Gln	Thr	Met	Glu	Gly	Val	Leu	Ser	Ala	Arg	Val
		115					120					125			
His	Ile	Ser	Tyr	Asp	Ile	Asp	Ala	Gly	Glu	Asn	Gly	Arg	Pro	Pro	Lys
130						135					140				
Pro	Val	His	Leu	Ser	Ala	Leu	Ala	Val	Tyr	Glu	Arg	Gly	Ser	Pro	Leu
145					150					155					160
Ala	His	Gln	Ile	Ser	Asp	Ile	Lys	Arg	Phe	Leu	Lys	Asn	Ser	Phe	Ala
				165					170					175	
Asp	Val	Asp	Tyr	Asp	Asn	Ile	Ser	Val	Val	Leu	Ser	Glu	Arg	Ser	Asp
			180					185					190		
Ala	Gln	Leu	Gln	Ala	Pro	Gly	Thr	Pro	Val	Lys	Arg	Asn	Ser	Phe	Ala
		195					200					205			
Thr	Ser	Trp	Ile	Val	Leu	Ile	Ile	Leu	Leu	Ser	Val	Met	Ser	Ala	Gly
		210				215					220				
Phe	Gly	Val	Trp	Tyr	Tyr	Lys	Asn	His	Tyr	Ala	Arg	Asn	Lys	Lys	Gly
225					230					235					240
Ile	Thr	Ala	Asp	Asp	Lys	Ala	Lys	Ser	Ser	Asn	Glu				
				245					250						

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Arg	Lys	Ala	Glu	Glu	Thr	Asn	Arg	Ile	Met	Gly	Cys	Ile	Gly	Lys	Val
1				5					10					15	
Leu	Gly	Ala	Leu	Leu	Thr	Ile	Val	Ser	Val	Val	Ala	Ala	Val	Phe	Thr
			20					25					30		
Gly	Gly	Ala	Ser	Leu	Ala	Leu	Ala	Ala	Val	Gly	Leu	Ala	Val	Met	Val
		35					40					45			
Ala	Asp	Glu	Ile	Val	Lys	Ala	Ala	Thr	Gly	Val	Ser	Phe	Ile	Gln	Gln
	50					55					60				
Ala	Leu	Asn	Pro	Ile	Met	Glu	His	Val	Leu	Lys	Pro	Leu	Met	Glu	Leu
65					70					75				80	
Ile	Gly	Lys	Ala	Ile	Thr	Lys	Ala	Leu	Glu	Gly	Leu	Gly	Val	Asp	Lys
			85						90					95	
Lys	Thr	Ala	Glu	Met	Ala	Gly	Ser	Ile	Val	Gly	Ala	Ile	Val	Ala	Ala
			100					105					110		
Ile	Ala	Met	Val	Ala	Val	Ile	Val	Val	Val	Ala	Val	Val	Gly	Lys	Gly
		115					120					125			
Ala	Ala	Ala	Lys	Leu	Gly	Asn	Ala	Leu	Ser	Lys	Met	Met	Gly	Glu	Thr
		130				135					140				
Ile	Lys	Lys	Leu	Val	Pro	Asn	Val	Leu	Lys	Gln	Leu	Ala	Gln	Asn	Gly
145					150					155					160
Ser	Lys	Leu	Phe	Thr	Gln	Gly	Met	Gln	Arg	Ile	Thr	Ser	Gly	Leu	Gly
			165						170					175	
Asn	Val	Gly	Ser	Lys	Met	Gly	Leu	Gln	Thr	Asn	Ala	Leu	Ser	Lys	Glu
			180					185					190		

Leu	Val	Gly	Asn	Thr	Leu	Asn	Lys	Val	Ala	Leu	Gly	Met	Glu	Val	Thr
		195					200					205			
Asn	Thr	Ala	Ala	Gln	Ser	Ala	Gly	Gly	Val	Ala	Glu	Gly	Val	Phe	Ile
	210					215					220				
Lys	Asn	Ala	Ser	Glu	Ala	Leu	Ala	Asp	Phe	Met	Leu	Ala	Arg	Phe	Ala
225					230					235					240
Met	Asp	Gln	Ile	Gln	Gln	Trp	Leu	Lys	Gln	Ser	Val	Glu	Ile	Phe	Gly
			245						250					255	
Glu	Asn	Gln	Lys	Val	Thr	Ala	Glu	Leu	Gln	Lys	Ala	Met	Ser	Ser	Ala
			260					265					270		
Val	Gln	Gln	Asn	Ala	Asp	Ala	Ser	Arg	Phe	Ile	Leu	Arg	Gln	Ser	Arg
		275					280					285			
Ala															

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Arg	Lys	Ala	Glu	Glu	Leu	Asn	Arg	Val	Met	Gly	Cys	Val	Gly	Lys	Ile
1				5					10					15	
Leu	Gly	Ala	Leu	Leu	Thr	Ile	Val	Ser	Val	Val	Ala	Ala	Ala	Phe	Ser
			20					25					30		
Gly	Gly	Ala	Ser	Leu	Ala	Leu	Ala	Ala	Val	Gly	Leu	Ala	Leu	Met	Val
		35				40						45			
Thr	Asp	Ala	Ile	Val	Gln	Ala	Ala	Thr	Gly	Asn	Ser	Phe	Met	Glu	Gln
	50					55					60				
Ala	Leu	Asn	Pro	Ile	Met	Lys	Ala	Val	Ile	Glu	Pro	Leu	Ile	Lys	Leu
	65				70					75					80
Leu	Ser	Asp	Ala	Phe	Thr	Lys	Met	Leu	Glu	Gly	Leu	Gly	Val	Asp	Ser
			85					90						95	
Lys	Lys	Ala	Lys	Met	Ile	Gly	Ser	Ile	Leu	Gly	Ala	Ile	Ala	Gly	Ala
		100						105					110		
Leu	Val	Leu	Val	Ala	Ala	Val	Val	Leu	Val	Ala	Thr	Val	Gly	Lys	Gln
	115					120						125			
Ala	Ala	Ala	Lys	Leu	Ala	Glu	Asn	Ile	Gly	Lys	Ile	Ile	Gly	Lys	Thr
	130				135						140				
Leu	Thr	Asp	Leu	Ile	Pro	Lys	Phe	Leu	Lys	Asn	Phe	Ser	Ser	Gln	Leu
145					150					155					160
Asp	Asp	Leu	Ile	Thr	Asn	Ala	Val	Ala	Arg	Leu	Asn	Lys	Phe	Leu	Gly
			165					170						175	
Ala	Ala	Gly	Asp	Glu	Val	Ile	Ser	Lys	Gln	Ile	Ile	Ser	Thr	His	Leu
		180					185						190		
Asn	Gln	Ala	Val	Leu	Leu	Gly	Glu	Ser	Val	Asn	Ser	Ala	Thr	Gln	Ala
	195					200						205			
Gly	Gly	Ser	Val	Ala	Ser	Ala	Val	Phe	Gln	Asn	Ser	Ala	Ser	Thr	Asn
	210					215					220				
Leu	Ala	Asp	Leu	Thr	Leu	Ser	Lys	Tyr	Gln	Val	Glu	Gln	Leu	Ser	Lys
225					230					235					240
Tyr	Ile	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Gly	Gln	Leu	Gln	Glu	Val	Ile
			245						250					255	
Ala	Asp	Leu	Leu	Ala	Ser	Met	Ser	Asn	Ser	Gln	Ala	Asn	Arg	Thr	Asp
		260						265					270		
Val	Ala	Lys	Ala	Ile	Leu	Gln	Gln	Thr	Thr	Ala					
		275					280								

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Leu	Ile	Ser	Asn	Val	Gly	Ile	Asn	Pro	Ala	Ala	Tyr	Leu	Asn	Asn	
1				5				10						15		
His	Ser	Val	Glu	Asn	Ser	Ser	Gln	Thr	Ala	Ser	Gln	Ser	Val	Ser	Ala	
			20					25					30			
Lys	Asp	Ile	Leu	Asn	Ser	Ile	Gly	Ile	Ser	Ser	Ser	Lys	Val	Ser	Asp	
			35				40					45				
Leu	Gly	Leu	Ser	Pro	Thr	Leu	Ser	Ala	Pro	Ala	Pro	Gly	Val	Leu	Thr	
	50					55					60					
Gln	Thr	Pro	Gly	Thr	Ile	Thr	Ser	Phe	Leu	Lys	Ala	Ser	Ile	Gln	Asn	
	65				70					75					80	
Thr	Asp	Met	Asn	Gln	Asp	Leu	Asn	Ala	Leu	Ala	Asn	Asn	Val	Thr	Thr	
			85					90						95		
Lys	Ala	Asn	Glu	Val	Val	Gln	Thr	Gln	Leu	Arg	Glu	Gln	Gln	Ala	Glu	
			100					105					110			
Val	Gly	Lys	Phe	Phe	Asp	Ile	Ser	Gly	Met	Ser	Ser	Ser	Ala	Val	Ala	
		115					120					125				
Leu	Leu	Ala	Ala	Ala	Asn	Thr	Leu	Met	Leu	Thr	Leu	Asn	Gln	Ala	Asp	
	130					135					140					
Ser	Lys	Leu	Ser	Gly	Lys	Leu	Ser	Leu	Val	Ser	Phe	Asp	Ala	Ala	Lys	
	145				150					155					160	
Thr	Thr	Ala	Ser	Ser	Met	Met	Arg	Glu	Gly	Met	Asn	Ala	Leu	Ser	Gly	
			165					170					175			
Ser	Ile	Ser	Gln	Ser	Ala	Leu	Gln	Leu	Gly	Ile	Thr	Gly	Val	Gly	Ala	
		180					185						190			
Lys	Leu	Glu	Tyr	Lys	Gly	Leu	Gln	Asn	Glu	Arg	Gly	Ala	Leu	Lys	His	
	195						200					205				
Asn	Ala	Ala	Lys	Ile	Asp	Lys	Leu	Thr	Thr	Glu	Ser	His	Ser	Ile	Lys	
	210					215					220					
Asn	Val	Leu	Asn	Gly	Gln	Asn	Ser	Val	Lys	Leu	Gly	Ala	Glu	Gly	Val	
	225			230					235						240	
Asp	Ser	Leu	Lys	Ser	Leu	Asn	Met	Lys	Lys	Thr	Gly	Thr	Asp	Ala	Thr	
			245					250						255		
Lys	Asn	Leu	Asn	Asp	Ala	Thr	Leu	Lys	Ser	Asn	Ala	Gly	Thr	Ser	Ala	
		260					265						270			
Thr	Glu	Ser	Leu	Gly	Ile	Lys	Asp	Ser	Asn	Lys	Gln	Ile	Ser	Pro	Glu	
	275					280						285				
His	Gln	Ala	Ile	Leu	Ser	Lys	Arg	Leu	Glu	Ser	Val	Glu	Ser	Asp	Ile	
	290					295					300					
Arg	Leu	Glu	Gln	Asn	Thr	Met	Asp	Met	Thr	Arg	Ile	Asp	Ala	Arg	Lys	
	305				310					315					320	
Met	Gln	Met	Thr	Gly	Asp	Leu	Ile	Met	Lys	Asn	Ser	Val	Thr	Val	Gly	
			325					330						335		
Gly	Ile	Ala	Gly	Ala	Ser	Gly	Gln	Tyr	Ala	Ala	Thr	Gln	Glu	Arg	Ser	
		340					345					350				
Glu	Gln	Gln	Ile	Ser	Gln	Val	Asn	Asn	Arg	Val	Ala	Ser	Thr	Ala	Ser	
	355					360					365					
Asp	Glu	Ala	Arg	Glu	Ser	Ser	Arg	Lys	Ser	Thr	Ser	Leu	Ile	Gln	Glu	
	370				375						380					
Met	Leu	Lys	Thr	Met	Glu	Ser	Ile	Asn	Gln	Ser	Lys	Ala	Ser	Ala	Leu	
	385				390					395					400	

Ala Ala Ile Ala Gly Asn Ile Arg Ala
405

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Leu	Gln	Lys	Gln	Phe	Cys	Asn	Lys	Leu	Leu	Leu	Asp	Thr	Asn	Lys	1	5	10	15
Glu	Asn	Val	Met	Glu	Ile	Gln	Asn	Thr	Lys	Pro	Thr	Gln	Thr	Leu	Tyr	20	25	30	
Thr	Asp	Ile	Ser	Thr	Lys	Gln	Thr	Gln	Ser	Ser	Ser	Glu	Thr	Gln	Lys	35	40	45	
Ser	Gln	Asn	Tyr	Gln	Gln	Ile	Ala	Ala	His	Ile	Pro	Leu	Asn	Val	Gly	50	55	60	
Lys	Asn	Pro	Val	Leu	Thr	Thr	Thr	Leu	Asn	Asp	Asp	Gln	Leu	Leu	Lys	65	70	75	80
Leu	Ser	Glu	Gln	Val	Gln	His	Asp	Ser	Glu	Ile	Ile	Ala	Arg	Leu	Thr	85	90	95	
Asp	Lys	Lys	Met	Lys	Asp	Leu	Ser	Glu	Met	Ser	His	Thr	Leu	Thr	Pro	100	105	110	
Glu	Asn	Thr	Leu	Asp	Ile	Ser	Ser	Leu	Ser	Ser	Asn	Ala	Val	Ser	Leu	115	120	125	
Ile	Ile	Ser	Val	Ala	Val	Leu	Leu	Ser	Ala	Leu	Arg	Thr	Ala	Glu	Thr	130	135	140	
Lys	Leu	Gly	Ser	Gln	Leu	Ser	Leu	Ile	Ala	Phe	Asp	Ala	Thr	Lys	Ser	145	150	155	160
Ala	Ala	Glu	Asn	Ile	Val	Arg	Gln	Gly	Leu	Ala	Ala	Leu	Ser	Ser	Ser	165	170	175	
Ile	Thr	Gly	Ala	Val	Thr	Gln	Val	Gly	Ile	Thr	Gly	Ile	Gly	Ala	Lys	180	185	190	
Lys	Thr	His	Ser	Gly	Ile	Ser	Asp	Gln	Lys	Gly	Ala	Leu	Arg	Lys	Asn	195	200	205	
Leu	Ala	Thr	Ala	Gln	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Gly	Ser	Lys	Leu	210	215	220	
Gly	Leu	Asn	Lys	Gln	Ile	Asp	Thr	Asn	Ile	Thr	Ser	Pro	Gln	Thr	Asn	225	230	235	240
Ser	Ser	Thr	Lys	Phe	Leu	Gly	Lys	Asn	Lys	Leu	Ala	Pro	Asp	Asn	Ile	245	250	255	
Ser	Leu	Ser	Thr	Glu	His	Lys	Thr	Ser	Leu	Ser	Ser	Pro	Asp	Ile	Ser	260	265	270	
Leu	Gln	Asp	Lys	Ile	Asp	Thr	Gln	Arg	Arg	Thr	Tyr	Glu	Leu	Asn	Thr	275	280	285	
Leu	Ser	Ala	Gln	Gln	Lys	Gln	Asn	Ile	Gly	Arg	Ala	Thr	Met	Glu	Thr	290	295	300	
Ser	Ala	Val	Ala	Gly	Asn	Ile	Ser	Thr	Ser	Gly	Gly	Arg	Tyr	Ala	Ser	305	310	315	320
Ala	Leu	Glu	Glu	Glu	Glu	Gln	Leu	Ile	Ser	Gln	Ala	Ser	Ser	Lys	Gln	325	330	335	
Ala	Glu	Glu	Ala	Ser	Gln	Val	Ser	Lys	Glu	Ala	Ser	Gln	Ala	Thr	Asn	340	345	350	
Gln	Leu	Ile	Gln	Lys	Leu	Leu	Asn	Ile	Ile	Asp	Ser	Ile	Asn	Gln	Ser	355	360	365	
Lys	Asn	Ser	Ala	Ala	Ser	Gln	Ile	Ala	Gly	Asn	Ile	Arg	Ala			370	375	380	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Leu	Asn	Ile	Gln	Asn	Tyr	Ser	Ala	Ser	Pro	His	Pro	Gly	Ile	Val
1				5					10					15	
Ala	Glu	Arg	Pro	Gln	Thr	Pro	Ser	Ala	Ser	Glu	His	Val	Glu	Thr	Ala
			20					25					30		
Val	Val	Pro	Ser	Thr	Thr	Glu	His	Arg	Gly	Thr	Asp	Ile	Ile	Ser	Leu
		35					40					45			
Ser	Gln	Ala	Ala	Thr	Lys	Ile	His	Gln	Ala	Gln	Gln	Thr	Leu	Gln	Ser
	50				55					60					
Thr	Pro	Pro	Ile	Ser	Glu	Glu	Asn	Asn	Asp	Glu	Arg	Thr	Leu	Ala	Arg
	65				70					75				80	
Gln	Gln	Leu	Thr	Ser	Ser	Leu	Asn	Ala	Leu	Ala	Lys	Ser	Gly	Val	Ser
				85					90					95	
Leu	Ser	Ala	Glu	Gln	Asn	Glu	Asn	Leu	Arg	Ser	Ala	Phe	Ser	Ala	Pro
		100						105				110			
Thr	Ser	Ala	Leu	Phe	Ser	Ala	Ser	Pro	Met	Ala	Gln	Pro	Arg	Thr	Thr
	115						120					125			
Ile	Ser	Asp	Ala	Glu	Ile	Trp	Asp	Met	Val	Ser	Gln	Asn	Ile	Ser	Ala
	130					135					140				
Ile	Gly	Asp	Ser	Tyr	Leu	Gly	Val	Tyr	Glu	Asn	Val	Val	Ala	Val	Tyr
	145				150					155				160	
Thr	Asp	Phe	Tyr	Gln	Ala	Phe	Ser	Asp	Ile	Leu	Ser	Lys	Met	Gly	Gly
				165					170					175	
Trp	Leu	Leu	Pro	Gly	Lys	Asp	Gly	Asn	Thr	Val	Lys	Leu	Asp	Val	Thr
		180					185						190		
Ser	Leu	Lys	Asn	Asp	Leu	Asn	Ser	Leu	Val	Asn	Lys	Tyr	Asn	Gln	Ile
		195					200					205			
Asn	Ser	Asn	Thr	Val	Leu	Phe	Pro	Ala	Gln	Ser	Gly	Ser	Gly	Val	Lys
	210					215					220				
Val	Ala	Thr	Glu	Ala	Glu	Ala	Arg	Gln	Trp	Leu	Ser	Glu	Leu	Asn	Leu
	225				230					235				240	
Pro	Asn	Ser	Cys	Leu	Lys	Ser	Tyr	Gly	Ser	Gly	Tyr	Val	Val	Thr	Val
			245						250					255	
Asp	Leu	Thr	Pro	Leu	Gln	Lys	Met	Val	Gln	Asp	Ile	Asp	Gly	Leu	Gly
		260						265					270		
Ala	Pro	Gly	Lys	Asp	Ser	Lys	Leu	Glu	Met	Asp	Asn	Ala	Lys	Tyr	Gln
	275						280					285			
Ala	Trp	Gln	Ser	Gly	Phe	Lys	Ala	Gln	Glu	Glu	Asn	Met	Lys	Thr	Thr
	290					295					300				
Leu	Gln	Thr	Leu	Thr	Gln	Lys	Tyr	Ser	Asn	Ala	Asn	Ser	Leu	Tyr	Asp
	305				310					315				320	
Asn	Leu	Val	Lys	Val	Leu	Ser	Ser	Thr	Ile	Ser	Ser	Ser	Leu	Glu	Thr
			325						330					335	
Ala	Lys	Ser	Phe	Leu	Gln	Gly									
			340												

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Asn	Ile	Thr	Thr	Leu	Thr	Asn	Ser	Ile	Ser	Thr	Ser	Ser	Phe	Ser
1				5					10					15	
Pro	Asn	Asn	Thr	Asn	Gly	Ser	Ser	Thr	Glu	Thr	Val	Asn	Ser	Asp	Ile
			20					25					30		
Lys	Thr	Thr	Thr	Ser	Ser	His	Pro	Val	Ser	Ser	Leu	Thr	Met	Leu	Asn
			35				40					45			
Asp	Thr	Leu	His	Asn	Ile	Arg	Thr	Thr	Asn	Gln	Ala	Leu	Lys	Lys	Glu
			50			55					60				
Leu	Ser	Gln	Lys	Thr	Leu	Thr	Lys	Thr	Ser	Leu	Glu	Glu	Ile	Ala	Leu
					70					75					80
His	Ser	Ser	Gln	Ile	Ser	Met	Asp	Val	Asn	Lys	Ser	Ala	Gln	Leu	Leu
				85					90					95	
Asp	Ile	Leu	Ser	Arg	Asn	Glu	Tyr	Pro	Ile	Asn	Lys	Asp	Ala	Arg	Glu
			100					105					110		
Leu	Leu	His	Ser	Ala	Pro	Lys	Glu	Ala	Glu	Leu	Asp	Gly	Asp	Gln	Met
			115				120					125			
Ile	Ser	His	Arg	Glu	Leu	Trp	Ala	Lys	Ile	Ala	Asn	Ser	Ile	Asn	Asp
						135						140			
Ile	Asn	Glu	Gln	Tyr	Leu	Lys	Val	Tyr	Glu	His	Ala	Val	Ser	Ser	Tyr
					150					155					160
Thr	Gln	Met	Tyr	Gln	Asp	Phe	Ser	Ala	Val	Leu	Ser	Ser	Leu	Ala	Gly
				165					170					175	
Trp	Ile	Ser	Pro	Gly	Gly	Asn	Asp	Gly	Asn	Ser	Val	Lys	Leu	Gln	Val
			180					185					190		
Asn	Ser	Leu	Lys	Lys	Ala	Leu	Glu	Glu	Leu	Lys	Glu	Lys	Tyr	Lys	Asp
			195				200					205			
Lys	Pro	Leu	Tyr	Pro	Ala	Asn	Asn	Thr	Val	Ser	Gln	Glu	Gln	Ala	Asn
			210			215					220				
Lys	Trp	Leu	Thr	Glu	Leu	Gly	Gly	Thr	Ile	Gly	Lys	Val	Ser	Gln	Lys
					230					235					240
Asn	Gly	Gly	Tyr	Val	Val	Ser	Ile	Asn	Met	Thr	Pro	Ile	Asp	Asn	Met
				245					250					255	
Leu	Lys	Ser	Leu	Asp	Asn	Leu	Gly	Gly	Asn	Gly	Glu	Val	Val	Leu	Asp
			260					265					270		
Asn	Ala	Lys	Tyr	Gln	Ala	Trp	Asn	Ala	Gly	Phe	Ser	Ala	Glu	Asp	Glu
			275				280					285			
Thr	Met	Lys	Asn	Asn	Leu	Gln	Thr	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ala
			290			295					300				
Asn	Ser	Ile	Phe	Asp	Asn	Leu	Val	Lys	Val	Leu	Ser	Ser	Thr	Ile	Ser
					310					315					320
Ser	Cys	Thr	Asp	Thr	Asp	Lys	Leu	Phe	Leu	His	Phe				
				325					330						

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Val	Thr	Ser	Val	Arg	Thr	Gln	Pro	Pro	Val	Ile	Met	Pro	Gly	Met
1				5					10					15	
Gln	Thr	Glu	Ile	Lys	Thr	Gln	Ala	Thr	Asn	Leu	Ala	Ala	Asn	Leu	Ser
			20					25						30	

Ala	Val	Arg	Glu	Ser	Ala	Thr	Ala	Thr	Leu	Ser	Gly	Glu	Ile	Lys	Gly
		35					40					45			
Pro	Gln	Leu	Glu	Asp	Phe	Pro	Ala	Leu	Ile	Lys	Gln	Ala	Ser	Leu	Asp
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TAGACGACTA TAGCTCTTGC T

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